



App No.: 10/046,649 10046649 . 102802
Title: Stress Proteins and Uses Therefor
Inventors: Richard A. Young, *et al.*

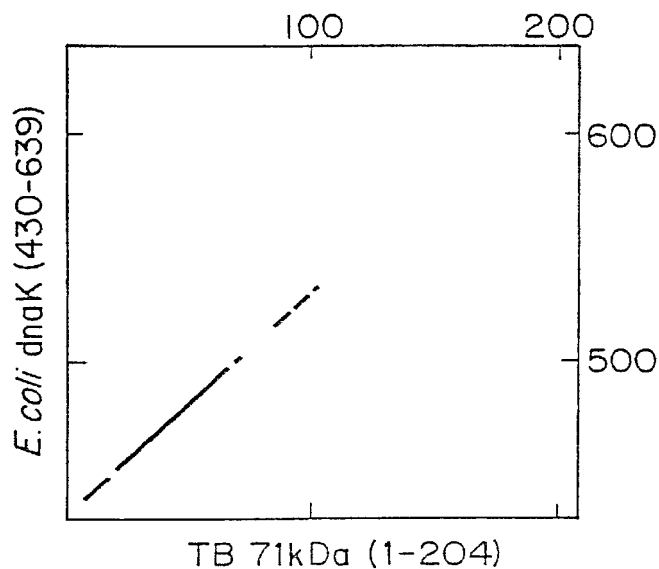


Fig. 1A

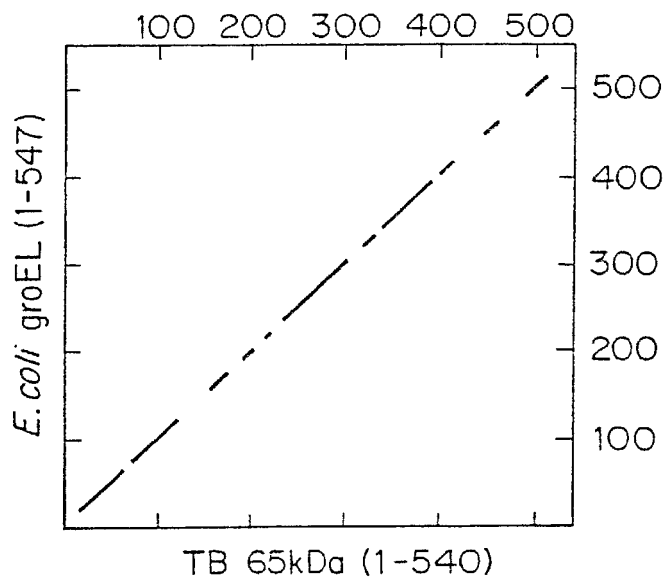
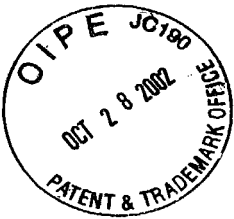


Fig. 1B



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1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRVILIEQSWGS						
GROEL	-----MA-----AKDVKFGNDARVKMLRGVNVVLADAVKVTGLGPKGRNVVLDKSFGA						
71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATATVLARSIAKEGFEKISKGANPVEI						
GROEL	PTITKDGVSVAEIEPEDKPFENMGAQNVKEVASKANDAAGDGTATATVLAQAIIITEGLKAVAAGMNPMDL						
141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVTIVKDGKTLNDE						
GROEL	RGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLIAEAMDVKVKEGVTIVEDGTGLQDE						
211	220	230	240	250	260	270	280
HUMP1	LEIIEGKMFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRRKPLVILAEVDVG						
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELES PFILLADKKISNIRENMLPVEAVAKAGKPLLIIEAEDVEG						
281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTLNLEDVQPHDLGKVGEVIV						
GROEL	EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGCTVISEE-IGMELEKATLEDLGQAARVVI						
351	360	370	380	390	400	410	420
HUMP1	TKDDANLLKGGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLVKGGTSDVEVNEKKDR						
GROEL	NKDDTTIIDGVGEEAAIQGRVAQIRQIEEATSDYDREKLQERVAKLGGVAVIKVGAATEVENKEKKAR						

Figure 2A



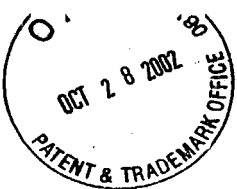
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421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPANTIAKNAGVEGSLI						
GROEL	VEDALHATRAAVEEGVAGGGVALIRVASKLADLRGQNEQNVSSSL-RAMEAPLRQIVLNCGEEPSVV						
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDANAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA						
GROEL	ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAAASVAGLMITTECMVTDLPKND-AADLGA						
561	570						
HUMP1	MGGMGG--GMGGGMF						
GROEL	AGGMGGMGGMGMM-						

Total score = 4667, 5 breaks
 276 identities out of 545 possible matches between residues

25 random runs
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

Figure 2B



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	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIIEQSWGS							
ML65K	M-----AKTIAYDEEARGLERGLNSLADAVKVTGLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLSIAKEGFEKISKGANPVEI							
ML65K	PTITNDGVSIKAEIELEDPEYKIGAEELVKEVAKTDDVAGDGTATVLAQALVKEGLRNVAAGANPLGL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
ML65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQ							
	211	220	230	240	250	260	270	280
HUMP1	LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSISIVPALEIANAHKPLVIAEDVDG							
ML65K	LELTEGMRFDKGYISGYFVTDARQEAQVLEEPYIILLVSSKVSTVKDLPPLLEKVIQAGKSLIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVLQVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTNLEDVQPHDLGKVGIV							
ML65K	EALSTLVVNKIRGTFKSVAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKGGDKAQIEKRIQEIIEIQLDVTTSEYEKEKLNERLAKLSGDGVAVLKVGTSDEVNEKKDR							
ML65K	TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDDYDREKLQERLAKLAGGVAVIKAGAAATEVELKERKHR							

Figure 3A



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421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIKRTLKIPAMTIAKNAGVEGSLI						
ML65K	IEDAVRNAAAVEEGIVAGGVTLQAAAPALDKLKLGTDEAT-GANIVKVALEAPLKQIAFNSGMEPGVV						
491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMA						
ML65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSAQNAAASIALGLFTT-EAVVADKPEKTAAPASDP						
561	570						
HUMP1	MGGMGGGGMGGMF						
ML65K	TGGMGG-MD---F						

Total score = 4552, 7 breaks
255 identities out of 540 possible matches between residues
25 random runs
Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.16

Figure 3B



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	1	10	20	30	40	50	60	70	
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIIEQSWGS								
TB65K	M-----AKTIAYDEEARRGLEGLNALADAVKVTGLGPKGRNVVLEKKWGA								
	71	80	90	100	110	120	130	140	
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATTATVLARSIAKEGFEKISKGANPVEI								
TB65K	PTITNDGVSIAKEIELEDPEYKIGAEELVKEVAKKTDVAGDGTATTATVLAQALRKEGLRNVAAGANPLGL								
	141	150	160	170	180	190	200	210	
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPPEELAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGTNLNDE								
TB65K	KRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISA-GDQSIGDLIAEANDKVGNEGVIIVEESNTFGLQ								
	211	220	230	240	250	260	270	280	
HUMP1	LEIIEGMKFDRCGYISPYFINTSKGQKCEFDQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG								
TB65K	LELTEGMRFDKGYISGYFVTDPERQEAILEDYPYILLVSSKSVSTVKDLLPLEKVGIGAGKPLIIAEDVEG								
	281	290	300	310	320	330	340	350	
HUMP1	EALSTLVNRLKVLQVAVKAPGFGDNRKNQLKDMAIATGAVFGEEGLTNLEDVQPHDLGKVGIV								
TB65K	EALSTLVVNKIRGTGFKSVAVKAPGFGDRRKAMLQDMAILTGQGVISEE-VGLTLENADLSLLGKARKVVV								
	351	360	370	380	390	400	410	420	
HUMP1	TKDDAMLLKKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR								
TB65K	TKDETTIVEGAGDTDIAIGRVAQIRQEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHR								

Figure 4A



App No.: 10/046,649 10046649 1002802
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	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIKRTLKIPAMTIKNAAGVEGSLI							
TB65K	IEDAVRNAKAAVEEGIVAGGGVTLQAAPTLDLQ-LEGDEATGANIVKVALEAPLKQIAFNSGLEPGVV							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNNMVEKGIIDPTKVVRTALLDAAAGVASLLTTAEVVVVTEIPKEEKDPGMGA							
TB65K	AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRTSALQNAASIAGLFLTTEAVVADKPEKEKASVPG-							
	561	570						
HUMP1	MGGMGGGGMGGMF							
TB65K	-----GGDMGGMDF							

Total score = 4560, 5 breaks
 257 identities out of 540 possible matches between residues

25 random runs
 Alignment score = 49.36 SD Standard deviation = 23.23 Mean = 3413.16

Figure 4B



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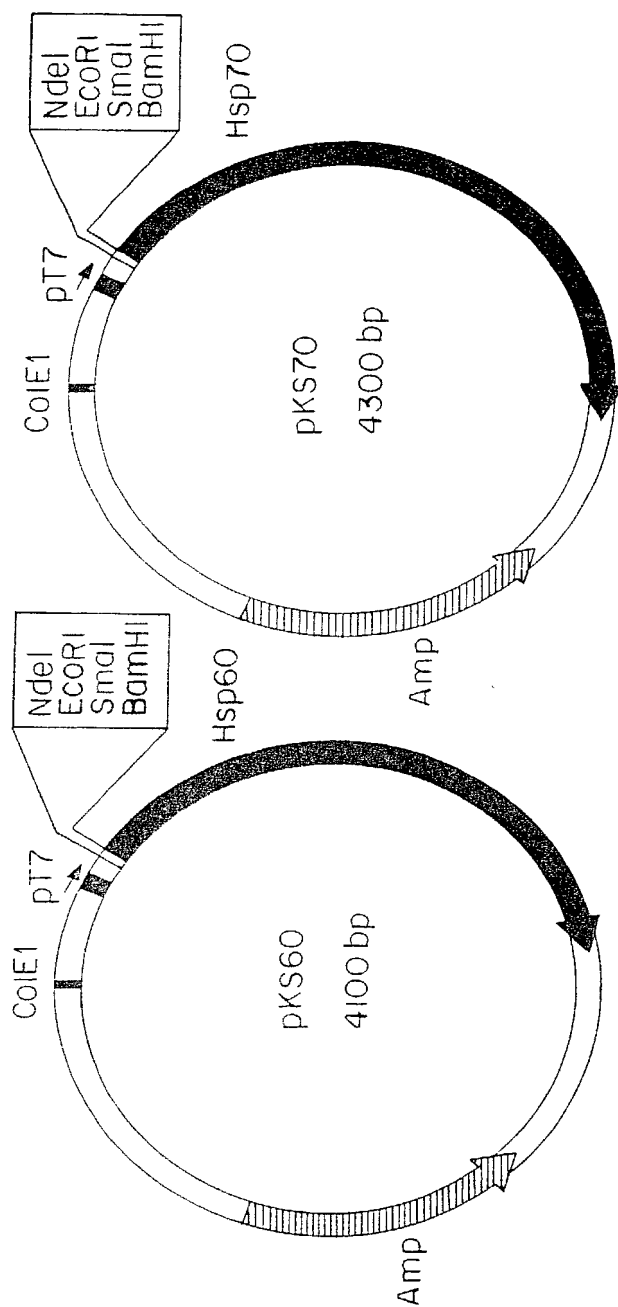


FIG. 5



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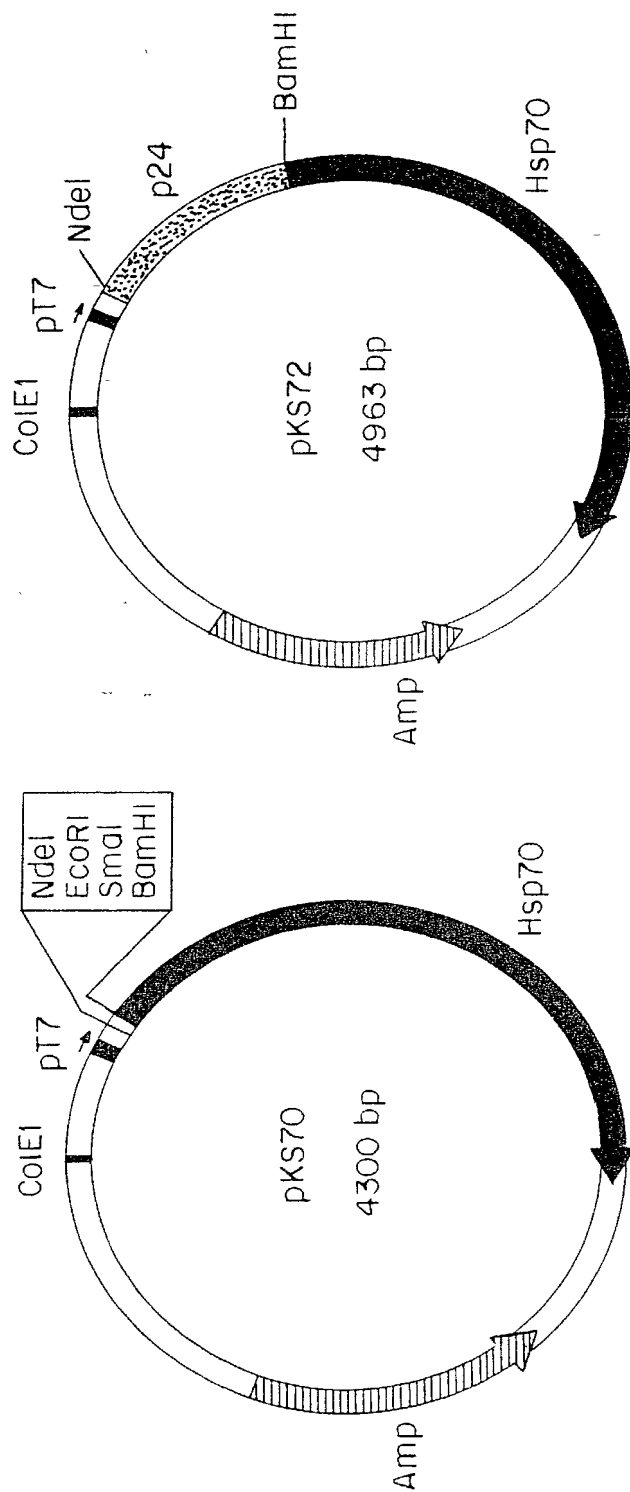


FIG. 6



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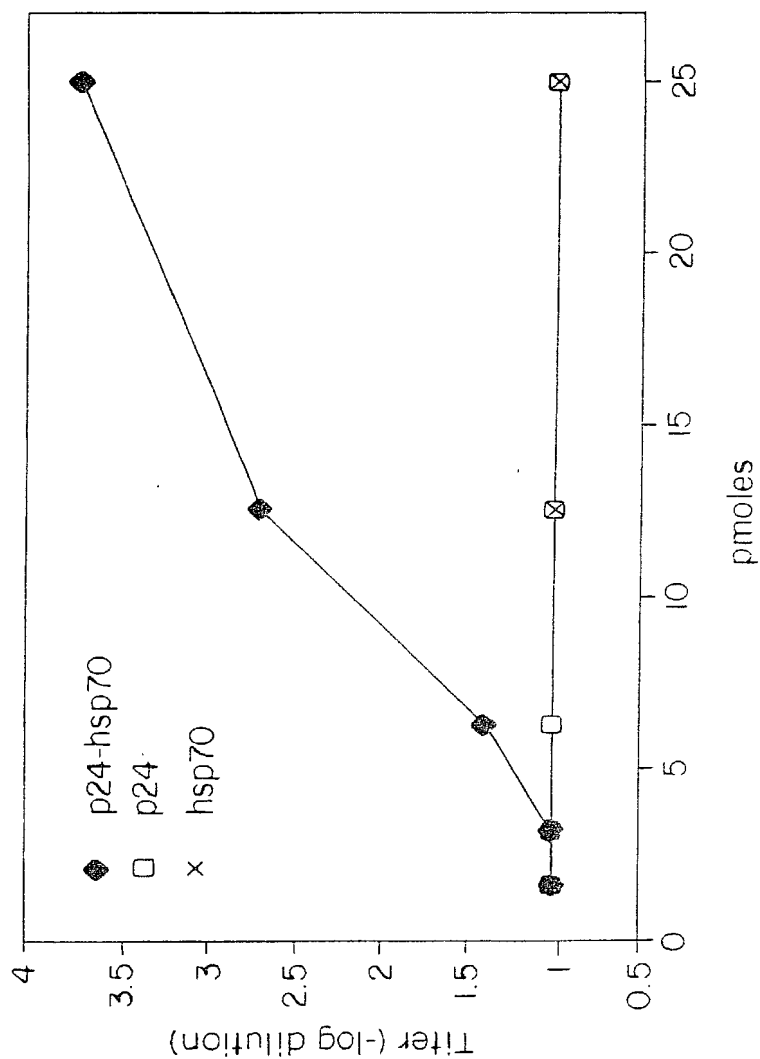


FIG. 7